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## SUMMARIES

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## ALIGNMENTS

			ORGANISM		SOURCE		REYMORDS	VERSION	ACCESSION		DEPINITION	POCIIS	RESULT 1 RATNIIAA	
Rateus	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Rattus norvegicus	male brain mRNA	Rattus norvegious (strain Sprague Dawley) (library: Stratagene)	synaptic protein.	alpha latroroxin; cell surface protoin; laminin; neurexin II-alpha;	M96376.1 GI:205714	M96376	(alternatively spliced) mRNAs, complete cds.	Rattus norvegious neutexin II-alpha major (non-proposed) and minor	PATNITAA 6436 bp mPNA linear POD 27-APP-1993		

REFERENCE

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PHATURES
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/rpt_family="A"
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/note="may be spliced out to produce alternative
C-terminal region for cds (ending at 6191)"
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/note="spliced region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nagase,T, Ishikawa,K, Suyama,M, Kikuno,B, Hirosawa,M., Miyajima,N, Tanaka,A, Kothani,H., Momura,M. and chara,O. Prediction of the coding sequences of unidentified human genes. XIII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro
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AB023139.2 GI.20521693
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Direct Submission
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OONDOSTOCTIMTS YGGSPOVIN POSTTY LEGACALITY TWP SAIDERSTRANDELAYGYS
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                    PPPVATRSPEVPPPPTFYPELTGVGATQDTLPPPAARRPPSGGECQAERINGSDCESPI
BASGEASGEVPDSSLPPTFIFIENFYTTFPLVTDFTTLLSPFKPAPRPULRTDGATGAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
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Post Local Similarity 86.3%,
Matches 41., Unservative
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    GHT40
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Submitted (125 NOV 1999) Naohiko Seki, Helik Research Instituto, Biological Technology Laboratory, Yana 1832-3, Kisarazu, Chita 291 0812, Japan (E-mailinsexishri.on.)p, Tel.91-438-52 1964, Pax:81 438-52-3952)
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neurexim II.
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Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo.
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EGSYQVOQSKAYISHSAGSMSAVVKEYAFAAFFTFYFAFFMYFYEYYV
4 1862 G 1766 J 906 C
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1. .6291
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                                                                /db_xref="taxon:9606"
                                                                                                        Location/Qualifiers
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LTVLARJEVGJURJAHOSHRIF KOREFHI ME HI HIL TRI REVISLEFSESGAGRGGAG

DVHQPTKGKEEFVATTKGNEF KOREFHI ME HI HIL TRI REVISLEFSESGAGRGGAG

DVHQTKGKEEFVATTKGNEF KOREFHI ME HI HIL TRI REVISLEMENTERLEGHAGI MALHTOKS HAM

DVHLISLKSGAVWLVIKUGS GAREAL WEF WIRZESTE FILGSEPTADLEGGEVONHMGG

LYDVVYKNIGEKLELSPLAFESI FYMFLOGELSFE TET VALLGEVTFRS PEAEVALPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC), 1-7-22 Suchire-chou, Tsurumi-ku, Yokohama, Kanagawa 230 045, Japan (B-mail-hartoriëgse riken go.jp., UEL-bitp://hgp.gsc_riken go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170
Cn Jan 13, 2001 this sequence version replaced gi-8117802
                                                                                                                                                                                                                                                                                                                                                                                                                                                order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae, Home.
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Consensus quality, 145474 bases at least Q40
Consensus quality, 148742 bases at least Q20
Consensus quality, 150150 bases, sum-of-contigs
Quality coverage: 8.51x in Q20 bases; sum-of-contigs
                                              104217
110864
116861
116769
125494
129024
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128923
132024
1326479
138454
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Project Information
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* NOTE: This is a "working draft' segmence It currently consists of 24 contigs. The true order of the piaces is not known and their order in this segmence record is
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* runs of N, but the exact sizes of the gaps are unknown
* This record will be updated with the finished sequence
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104117 104216: gap of
104117 104216: gap of
104217 110763: conti-
110764 11000
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120669 120768; gap of 100 bp
120769 125393; contig of 4625 bp in length
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150847 150946: gap of 108:
152047 15127: gap of 100 k
152128 153169 gaprig of 1042
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138455 138554: gap of 100 bp
138555 141639: contig of 3085 bp in length
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125494 128923: cont.g of 3430 bp
128824 129023: gap of 100 bp
128824 129023: gap of 100 bp
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                             20993.
  /note="assembly_fragment"
                                                                                                                                                                                      /organism="Homo sapiens"
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                                                                                             /clone="RP11-727K3"
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42201: contig of 9881 bp in length
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Submitted (15-MAR-COON MARANITA BATTIE), The Incrittute of Physical and Obemical Research (BEMEN), Genomic Sciences Center (MSC); Mitasaro Univ, 1-15-1 Kitasaro, Sagamihara, Kanadawa 228-8555, Mapan (B-mail: Hattoriägscirken.go.jp, URL-http://hdp.gsc.riken.go.jp/, Tel:81-42-778-9924)
Con May 33, 0000 tillo arguette Mersits replaced gi.7262597.
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Hatteri,M., Ishii,V., Toyoda,A., Taylor,T.D., Hong-Seog,P.
Pujiyama,A., Yada,T., Totoki,Y., Waranaho,H. and Sakaki,Y.
Homo sapiens 157,454 genomic DNA of 11q13

Published (bi) in Fatabase (2009)

Chases 1 to 157454)

Hattori,M., Ishii,V., Toyoda,A., Taylor,T.D., Hong-Seog,P.
Pujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Mammalia, Eutheria, Primateo, Catarrhini, Hominidae, Homo.
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Security: Dye-terminator ET-amersham, 100% of reads
Chemistry: Dye-terminator ET-amersham, 100% of reads
Assembly program: Phrap, version o eq0329
Consensus quality: 120400 hares at least Q40
Consensus quality: 140500 hases at least Q30
Consensus quality: 150042 bases at least Q30
Consensus quality: 150042
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Contact: hattori@gsc riken.go.jp
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Sequence updated (26.M3y 2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 33 contigs. The true order of the pieces
* is not known and their order in this sequence record is
130915 132593 contig of 1679 bp in length 132594 132694; gap of 100 bp in length 132694 134516; contig of 1823 bp in length 134517 134616; gap of 100 bp in length 137107 13720c. gap of 2490 bp in length 137207 140498; connig of 2490 bp in length 137207 140498; connig of 3200 bp in length 140499 140594; gap of 100 bp
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53053: contig of 10624 bp in length
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53154. .63766
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Mammalia, Euthoria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 164735)
Birron, B., Lincon, L., Nucbaum, C. and Landor, E.
Homo, Sapiens chromosome 11, clone RP11-141721
                                                                                                                                                                                                                                                                                                                                      All repeats were identified using PereatMacker
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-PEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On, 701-11, 2001 this segmence version replaced gi 13059473.
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Assembly program. Phiap, version 0.96031
                                                                                                            Center clone name: 141 J 21
                                                                                                                              Contact: sequence_submissionskyenome wi mit.edu
------ Project Information
Center project name: L12422
                                                                                                                                                                                                          Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                        Center code: WIBR
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Consensus quality: 159435 bases at least Q40 consensus quality: 161846 bases at least Q30 consensus quality: 162867 bases at least Q20 linsert size: 168000; againse-fp linsert size: 168000; againse-fp linsert size: 163435; sum-of-contigs for the process of the
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\* NOTE. This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will 2587 2722 2551126 kp in length 2522 2551126 kp in length 2722 3822 2551126 kp in length 2722 3822 25512 c5 1126 kp in length 2823 4832 25512 100 kp in length 4933 5032; gap of 100 kp in length 5033 6375; contig of 1343 kp in length 6376 6475 gap of 100 kp f476 6476 READ2 READ: gap of 100 hr 2599 11774 117843 gap of 100 hp in length 117744 117843 gap of 100 hp 117944 160670 contig of 42006 hp in length 160640 160670 gap of 100 hp 160640 164778 contig of 4006 hp in length. 100 bp in length 100 bp 88891; contig of 11373 bp in length 88892 88991; contig of 11373 bp in length 98992 88991; gap of 100 kg 11940 57508: contig of 45569 bp in length 57509 57608: gap of 100 bp 57609 66235: contig of 8627 bp in length 66236 66315: gap of 100 bp 66336 66315: gap of 8083 bp in length 66336 74418: contig of 8083 bp in length 5033 6,475; cource 100 bp 6376 6475; gap of 100 bp 6476 792c; contig of 1450 bp in length 7926 8026; gap of 100 bp 10 length 8026 11839; contig of 3814 bp in length 100 bp 100 length 100 bp 100 length 100 bp 100 length 100 bp 100 length 100 l Gaps between the coutigs are represented as 1813: contig of 1813 bp in length of 100 bp ' continues of 573 bp in length

Institute Pattle, WA

90% of reads

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REFERENCE
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[A control of the 
Powen, L., Madan, A., Qin, S., Baradarani, L., Birditt, B., Bloom Burke, J., Dors, M., Fleetwood, P., Kaur, A., Madan, A., Nesbitt, Pate, D. and Hood, L.
                                                                                                                 Lives Schmisses:
Submitted (12 APP 2000) Mulrimegabase Sequencing Center, University of Washington, po Box 357730, Seattle, WA 98195, USA
3 (bases 1 to 170114)
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Blocm, C., Cars, M., Dickloff, P., Flee, woold, D., Harrison, G.,
James, R., Faur, A., Mudan, A., Gwen, M.P., Faralliffe, A., Shaffet, T.
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                                                                                       .m.o.o.la
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On Jun 28, 2001 this sequence wersion replayed 3: 11120754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing vector: prola; 108752
Chemistry: Dye-terminator Big Dye; 90% of
Chemistry: Dye-terminator Big Tye, 10% of rea
Assembly program: Phrap; version 0 990399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://chroma.mbt.washington.edu/msg_Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Multimegabase Sequencing Center Center code: UWMSC
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/note="low quality
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/clone="RP11-141J21"
/clone=lik="PPCT bin=an BAC library 11"
/nothe="Data from overlapping RACs 13707 ACOA0134 and PPS-1045021 ACO12153 was added and the consensus sequence was determined from RP11-141J21 ACO44730 to the extent
                                                                                                                                                                                               alpha transcript."

3010(4111 4840),00007. 200074.20123 20100,07507 075

30502 47674 41676,4775 42686 7671 77740,

68860 577446,57464 67867,64777 64300,65947 67864,

68860 57746,57464 67867,64777 64300,65947 67864,

687646 87764,87867,91446 71676,94400 76745,

97626 97704,100916, 100802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /Hote-"Neurexin II has a promoter in an intron which generates mena for the shorter beta form. Based on alignment to rat opna mega77, the transcript begins at position 74684. The ATC start codon for the first exon of beta is at position 75195 and the exon ends at 75459.
                                                                              /note-"neurexin 2 alpha gene product; Exon 1, a s/
untranslated exon is not in this clone but is in BAC clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This exon is in the intron between exons 17 and 18 of the
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/db_xr≈f="taxon-9606"
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2520. .2580
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/codon_start=1
                                               13707 AC000134"
                                                                                                                                                                     /gene="NRXN2"
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70749, 65964, 59780,

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MKIMI PARMITERADVSIDEMSGRAYGIMMATTSRESADTILBUELDGQQMKITVALLO
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EHNIG SEK GEGENTERASHKIHNEMHTVREVERGKSI-GLSUVATVEGGMKAHMALE
EHNIG KROCABEKGPETTEFANHKIHNEMHTVREVERGKSI-GLSUVATVEGGMKAHMALE
ENDA EKTERFETS VERKENISE IGHIL OGUNEND GEGENTÄTTATOLLILENGOSGUNET VER
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GYLHYVEDLISMES LIMKENSEK EVNICHMENVAVS FORSIVHTLKILISKTVTGHSNAA
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ENILDIK SELVI IGGIL SELMKENSETHERSTEHGE SAVLVEVESASGLODVICHHIGGIVAVI E FY SAM
LITYTMEPRIND FORDMODELAVGESTHERS SAMLVEVESASGLODVICHHIGGIVATUVAGLEV
IALAAESDENVENDERLIKOSGERS VILLS ABSTRATTLANAMITTIMETTETTMATTITPP
PRESETLERSTTANDOLLVASAAC PSODERLEEGEBSTGGELIED ITTEGSIN PRV
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ATTESPEVERFELTGVANGACHILIPPEARS PRESONETGREPETESCTEEPIEAS
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LEDVVYKNNDEKLELSRLAKEGGEMALGELLSEKGELVALLENTTESSEEAFVALLE
WSAKTTOSTELLDERTKENGLLEGGEMENGENSESGASSESAGARVEAKELLEGHLYL
LDMASSGIKLEASSEKTENGIEMENGERGEBENGSTENSKOSTEFLATMELLEGHLYE
ELYLGGIDEGGEVOLFEREWTAALRAGYVGEVERTETGESEFFLEGLAEAGGAVGV
APECSPETIKGGASAFGPNGGVGEGMNEFTGEGTTGGELGPVGEPATVLSVGSMY
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DVHQPTKSKEEFVATEKSNEFFCYSLSHNEIGSSTEEITLAFRTLGPNSLALHTSKSA
DYVNLSLKSJAVMLVINGSSAFEALVEITVNSKEHDNAMHSVEVEVIRILEQHAGISHAM
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LSALTISTVKKEPPFFBGLLANLKLGEFFPALLGSGGIPGATARFUCAFAFNPGANGGL
LSALTISTVKKEPPFFBGLLANLKLGEFFPALLGSGGIPGATARFUCAFAFNPGANGGL
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/note="low quality data"
74540...74681
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PSAFAFKLI A JEXKHRDED JE LLEWED JPDARTSEEL BEELFEDVISAFGETHUF
TANPTGPGERGPPGAVEVIRESSSTTGMVVGIVAAAALCILILLYAMYKYRNRDEGSV
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74969, 74997
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74816. .74828
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                                                                          /gene-"NPXN2"
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77101. .77110
                                                                                                                                                                                         /gene="NRXN2"
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2 (bases i in import Nusbaum, California Musbaum, California Musba
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Mammalia; Eutheria; Primates;
1 (bases 1 to 196591)
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HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Homo sapiens
                                                                                                                                                       Unpublished
2 (bases 1 to 196591)
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Homo sapiens chromosome 11, clone RP11-869B15
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//db_xref="GL:145/3667"
//db_xref="GL:145/3667"
//td_xref="GL:145/3667"
//td_abs_at_lon="makestledly-seldengengepengepengepengegelden ALTERNASSELLEDEN ALTERNASSELTEN ALTERN
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complement (juin(116447...116510,117960...117263,
117927...11921,119219...118720,119070...119199,
117939...119482,1194195...104363,1194499...124593,
109116...10910,1196447...1104363,1194499...126116...109119...109119...109119...1196441))
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/product="RST"
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110547. .170114
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87.6%; Pred No. 2.8e-55;
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Catarrhini, Hominidae, Homo.
                                                          Lander, E., Allen, N., Anderson,
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Lamazares, P. Landers, T. Lehnczky, J. Levine, R., Liu, G.,
MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M.,
McEwan, P., McFernan, K., McPheeters, P., Moldrim, J., Menens, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nayyen, C., Norbu, C.,
Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Peterson, K., Phunkhang, P., Piere, N., Pollara, V., Raymond, C.,
Petta, P., Pieback, M., Piley, P., Rise, C., Pogov, P., Roman, J.,
Posetti, M., Poy, A., Santos, P., Schauer, S., Schupback, P., Seaman, S.,
Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S.,
Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, P., Vo, A., Wilson, H., Wu, X., Wyman, D., Ye, W. T., Young, G.,
Dairoot, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (28 MAP-2001) Whitehead Institute/MIT Center for Senome Submitted (28 MAP-2001) Whitehead Institute/MIT Center for Senome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sen 20, 2001 this segmence version replaced gi 10024642 on Sen 20, 2001 this segmence version replaced gi 10024642 on Senot were identified using RepeatMasker:

All repeats were identified using RepeatMasker html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome_washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
1501 1600 gap of 100 bp 100 1601 3902: contig of 2302 bp in length 3903 4002 gap of 100 bp 4003 4002 gap of 100 bp 100 6847 6946 gap of 100 bp 1233 13038; gap of 100 bp 1233 252; contig of 8494 bp in length 1233 252; contig of 8494 bp in length 1233 262; contig of 8494 bp in length 160 bp 160 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome_wi.mit edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: Flasmid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center clone name: 869_B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq wi.mit edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 602. gap of 100 bp
603 1500: contig of 898 bp in length
1501 1600: gap of 100 bp
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The University Of Okiahoma, 620 Farrington Oval, Room 209, Norman
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                                                                                                                                                                                                                  The University Of Oklahoma, OK 73019, USA 10 (bases 1 to 203300)
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Submitted (24-AFR 1999) Department Cf Chemistry And Brockemistry,
The University of Oklanoma, 600 Parrington Wil, From 208, Norman,
OK 73019, USA
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Submitted (23-MAP-1999) Department Of Chemistry And Biochemistry,
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OK 73019, USA
12 (bases 1 to 203300)
             Direct Submission
Submitted (14 MAY 1999) Department
The University of Skiahowa, (27 Fig
OK 73019, USA
                                                                                       Roe, B.A.
                                                                                                                                         Cutesteed (Di-MAY 1956) Tepartment of Chemistry And Biothemistry, The University Of Oklahoma, 620 Parkington Oval, Form 208, Norman
                                                                                                                                                                               Direct Submission
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                                                                                                                                                                                                                                                      Sabmitted 199 AFF-1979. Department of Themistry And Biochemistry, The University Of Oklahoma, 629 Farrington Oval, Form 178, Morman,
                                                                                                                                                                                                                                                                                       Direct Submission
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Submitted (05-MAY-1999) Department Of Chemistry And Blochemistry,
The University Of Taklahoma, F20 Particytes Oval, Fcom 208, Norman,
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Seki,M., Yoshikawa,T., Aduma,T., Sairo,T. and Moramatsu,M.
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292-0812, Japan (E.wail:nsekiehri.co Sp. Tel-91 478 52-3964)
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Homo sapiens mFNA for KIAA0578 protein, partial
AB011150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Syle:17-4 (1 985-198) (samu chata, Fazusa ENA besearch Institute,
Lakiastry of CNA Technology, Yana 1990-2, Figurazu, Chita
200 0810, Japan (E mail.udmainfoakarusa.rr.jp, Tel.-81-423-52-391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax:+81-438-52-3914)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/product="KIAA0578 protein"
/protein_id="PAA25594_2"
/brozein_id="SAPA859"
/translation="RPAHPSHSPLSPYLSVS_EPPYEPVTVSFTILTESAPAPPPFTFA
                                                                                                                                                                                                                                                                                                                                                         tissue type "brain"
/clone_Lbs "pBCSKFOW"
/note= "This sequence was replaced that of highland CDNA as a representative cDNA sequence for KIAAO578."
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                                                                                                                                                              /gene="KIAA0578"
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Submitted (19-10:T1948) (Samu Thara, Karusa ENA Research Institute,
Submitted (19-10:T1948) (Samu Thara, Karusa ENA Research Institute,
Laboratory of DNA Technology; Yana 1532-3, Kisarazu, Chiba
292-1917, [apar (E-mail odnalis5/8karusa av jr. Tele+91 438 52-1011,
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AQSNGTLMKEKQESSKEGHKKQENKLEEVYV"
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ISVVPSSFI GHUGSLMENGLEVIDLCKNGDLINVGELKAFGLEN I ADDVITFTYSSY
LSLATUQAYISMHLEFDGENTYSPGFILLENSDGHDE YAVELVYGYYHVYCELSDYGPH
VIXGHSGFELNENGLEVITTPENSHTHSI FVDTTVVTQVIHJAFNILLINGSLIYAN I
AQGMYSNLPKLVASPGGFG-1-LASVOLM-PLFOLINDAHPS-9-JIKFG-EGFSTTCQE
DSCANQGVCMQCMEGTFCDCOSMTS-SSONQCNDPGATY-IFGKSGGLILIXTMPANILERSI
RSDFLAVGFETYVFGJLVPIDSAPGLJDFLQLHIEQGFIGVVFNIGTVDISIFEEPT
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QKFANIDGEMYHDTIQEEDSRSGTISVNSPRTFFTAGGESELLTLEGENYLLGELFSAKCTG
LIPTELWTAMLNYGYVJSIRELFIGGSFKNIRQLARMQNAAGSVGSSSMSAKCTG
YPCKNNAVCKOGWNFFIGDTGTGTGVWGFTCEREASISKYDGSMYMKIIMPMVMHTDSE
DVSFRFMSQBAYGLLVATTSPDSADTLFLELDGGPVKLMVNLDGTFINGNSSKGPETL
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                                                                         CTATSANSSATSTANSCATSTANAGATSAAGATSATSSATSATSCATASSANSCAGA 433
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Sequence 11 from Parent W00194587
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si,Y., Bandman,O., Tang,Y.T., Lu,Y., Baughn,M.P., Duggan,B.M.,
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Hafalia,A. and Policky,√ L
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Ullifich, B., Ushkaryov, Y.A. and Sudhof, T.C.
Carrography of neuroxins more than 1990 (soforms generated by
alternative splicing and expressed in distinct subsets of neurons
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea
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SPVSINEMGGLEVVLYKNÖVELLESLAKOGDENMILHGVVAREGENVATLEFITE
EPESFISLDEMNAKFTGSI SFOFFTTEPNGLILIFSHGKPÞHQKDAKHPQMI KVDFEAI
EMLDGHLYLLLOMGSGTI KI KALÇKKVNEGEWYHVTPÓFFÖRÐSTT SVNTLÆTEYTAF
GESGLI-LELDGELYLGGLEVLKANLOKENLENGTALLNYGYVGTI FÖLFILGGGEDELEQI
NAGVSI IAÐVKÞSK-SEFILKFOLSNFKNOM FILMHYDYNFO-TSGTTYLDFSGEREAI
VLSYDGSMEMEI QLEVVMHTEAEDVSLÞFBSQÐAYGILMATTSÞPRSADTI ÞELDAGÐ
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AGEEGBOGUCLNOGUGSERTTATEFGSETGFFOFTTGSGETNUEGGLAHLMMGDGGSS
KECHNESTALMGGGGGGETTATEFGSETGSFTGFFOTTLGFFTLGFFTLGFFT
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LLTDTPVNDSAWHNVBTRRGEPNTTLETTYVERAWVEXESKEPRMTVESGLEVSGEPAT
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